Figure 1

Spacing Between Adjacent Peaks in the Raw Data
(M13, T's T=6%, 60C, Long Gel)
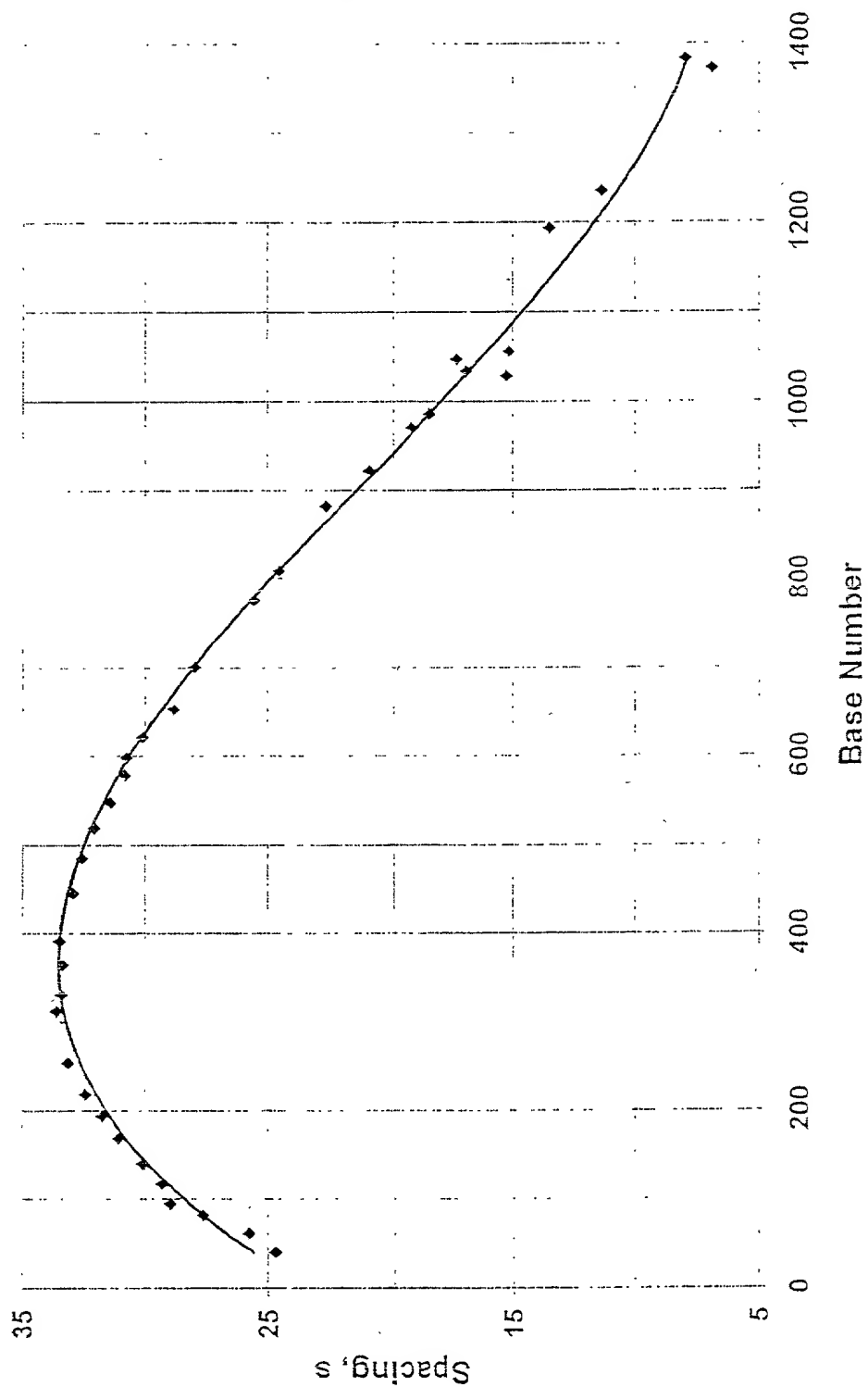
Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data)
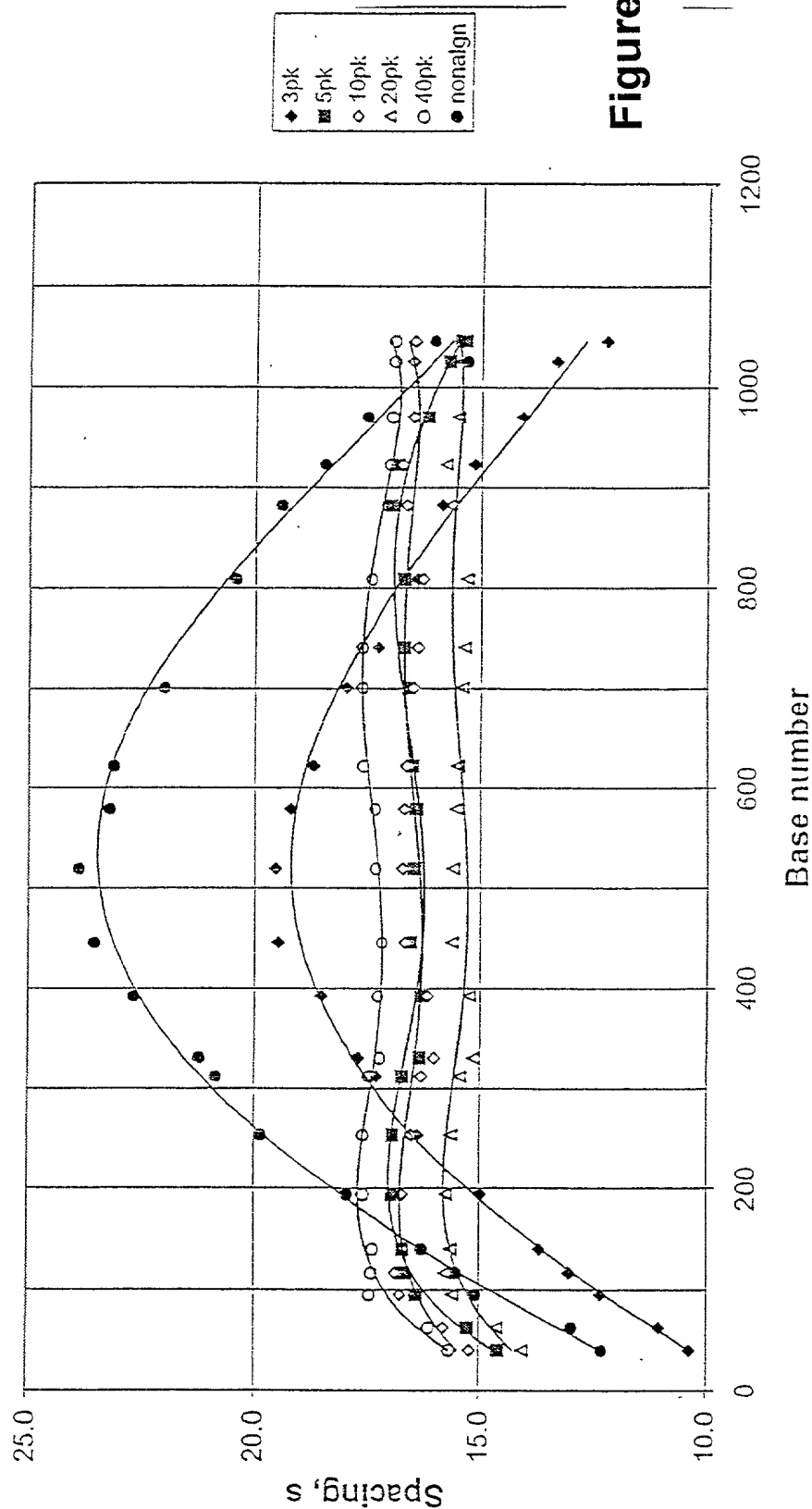(M13, Long Gel, 55C, T=6%)

Figure 2

Standard Deviation (%) of the Spacing Between Adjacent Bases from Average as a Function of Number of Peaks Used as a Reference for Alignment of Raw Data
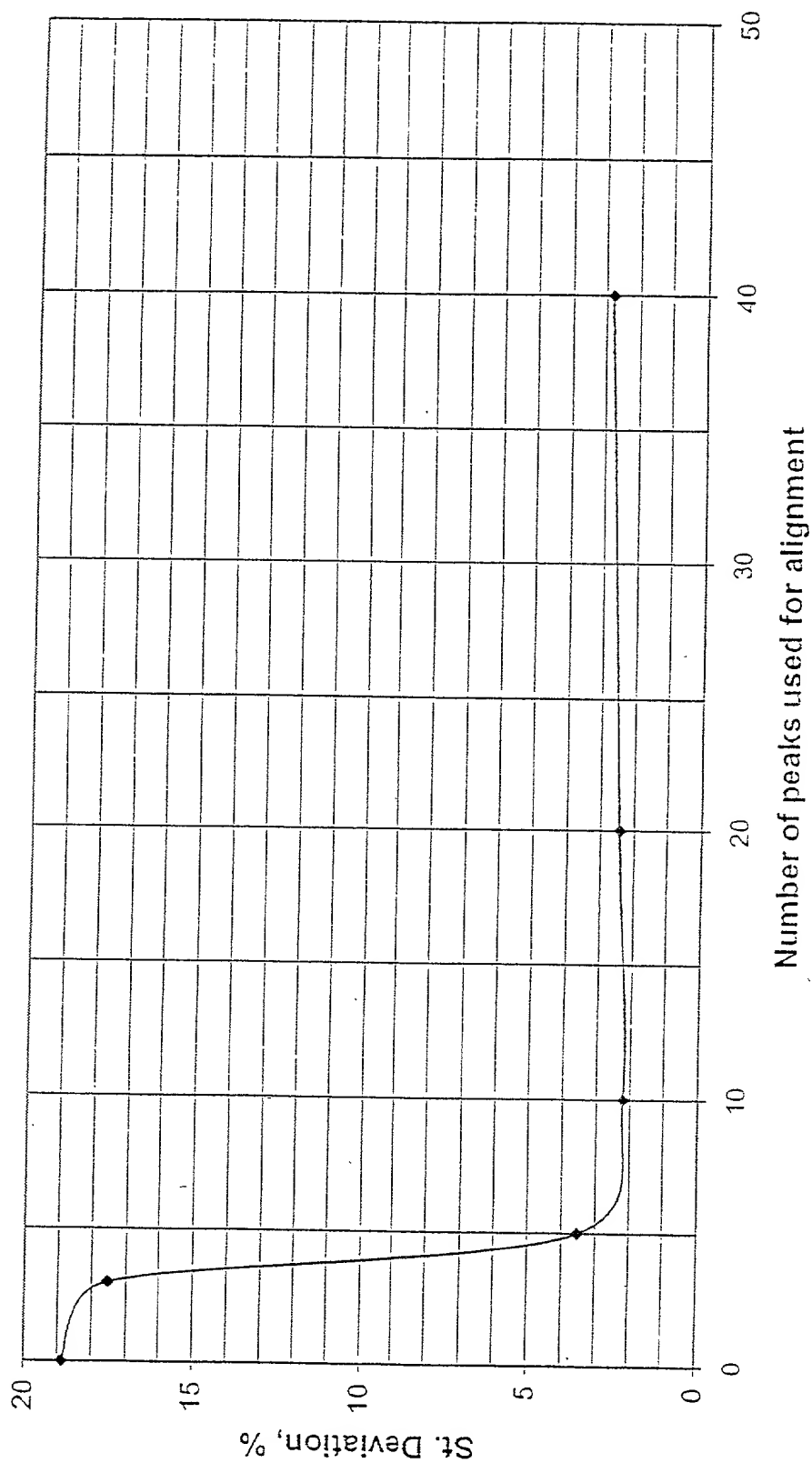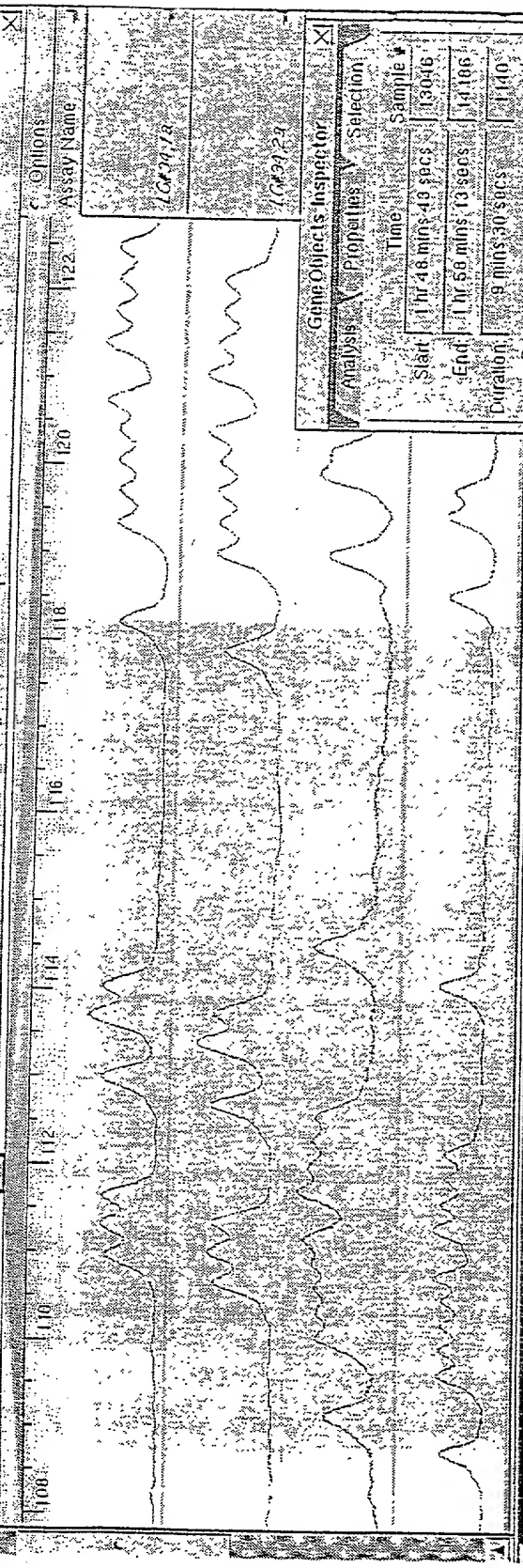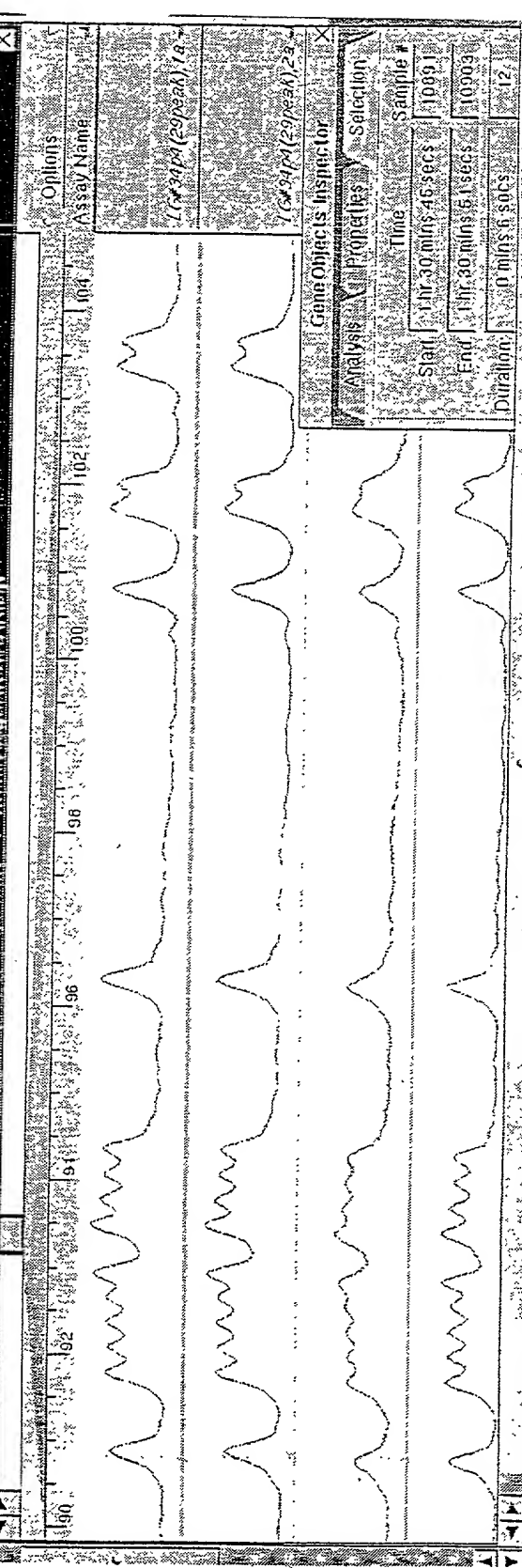

Number of peaks used for alignment

St. Deviation, %

Figure 3

Figure 4

Run Time of the BP#1056 in Different Lanes
(after alignment based on 10 peaks)
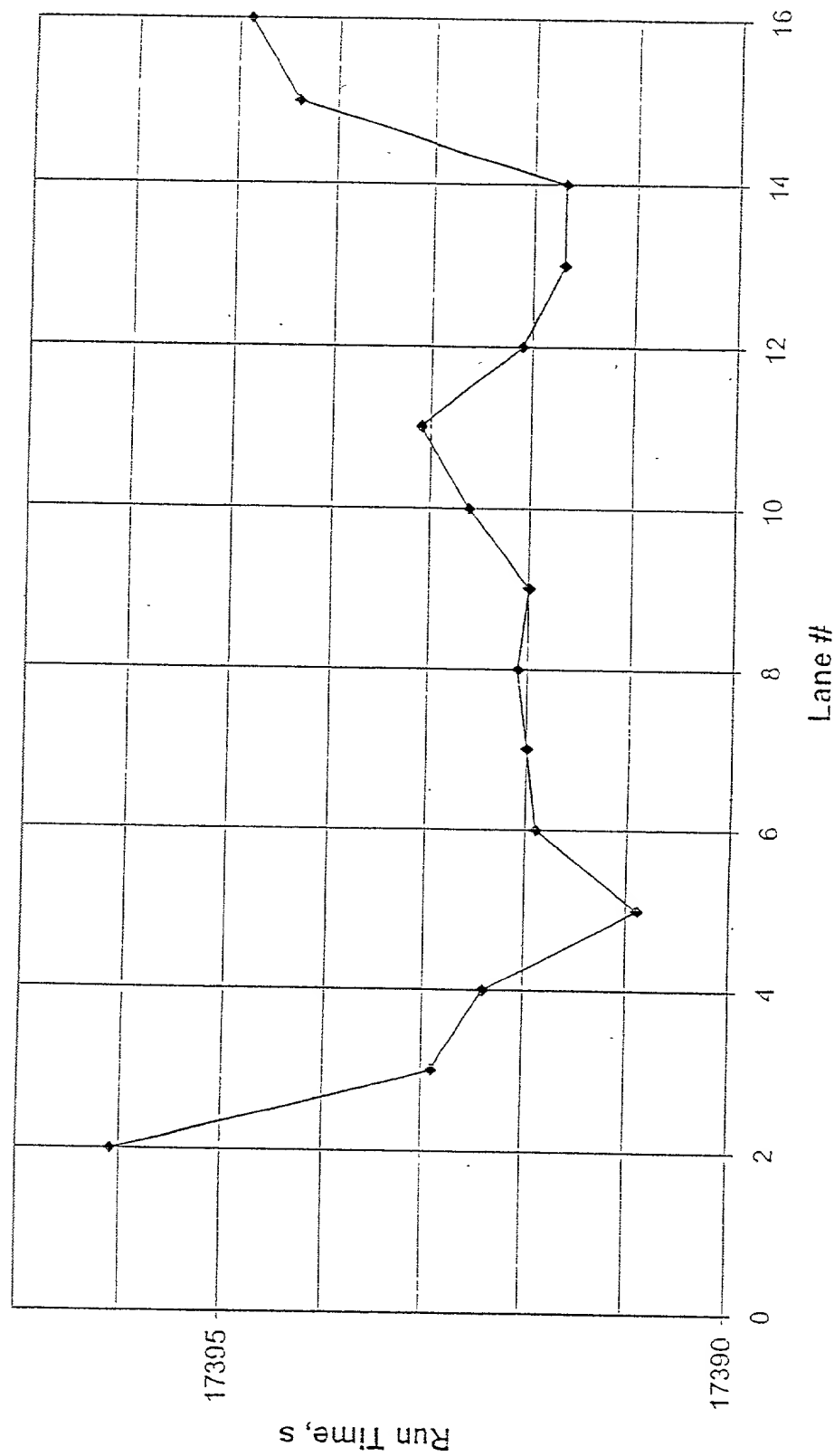
Figure 5

Figure 6

Figure 7

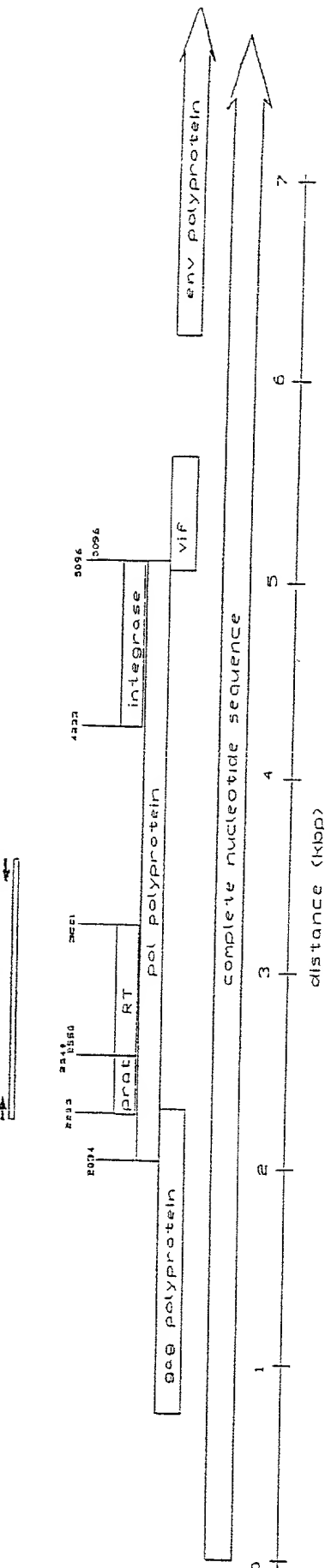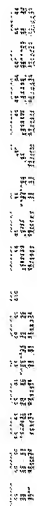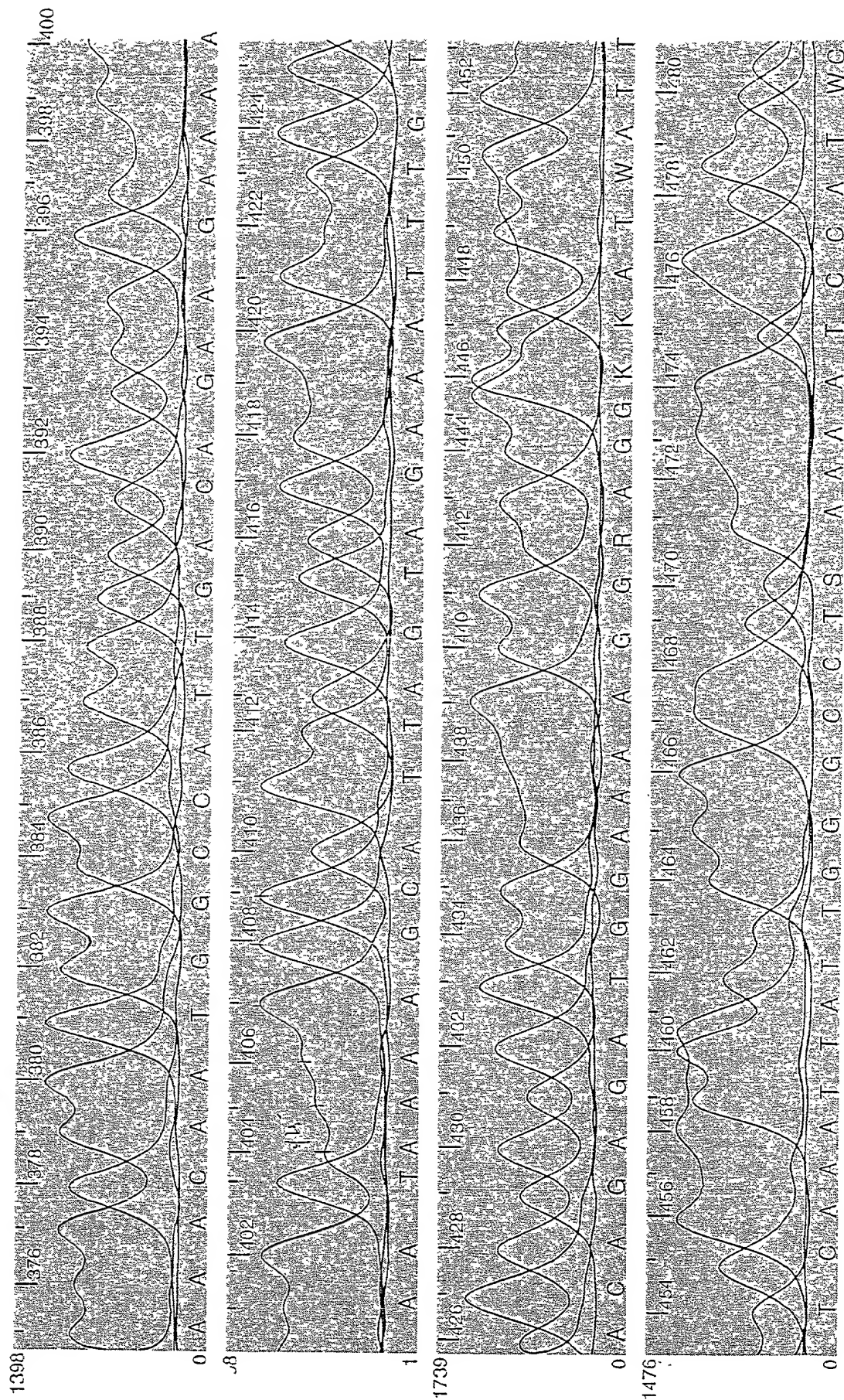Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Figure 8

Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Block #1 - intervening block

Block #2 - alignment block

Block #3 - intervening block

Block #4 - alignment block

Block #5 - intervening

Block #6 - alignment block

Block #7 - intervening block

Block #8 - alignment block

Figure 9A

Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

Figure 9B

Figure 9C

Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc
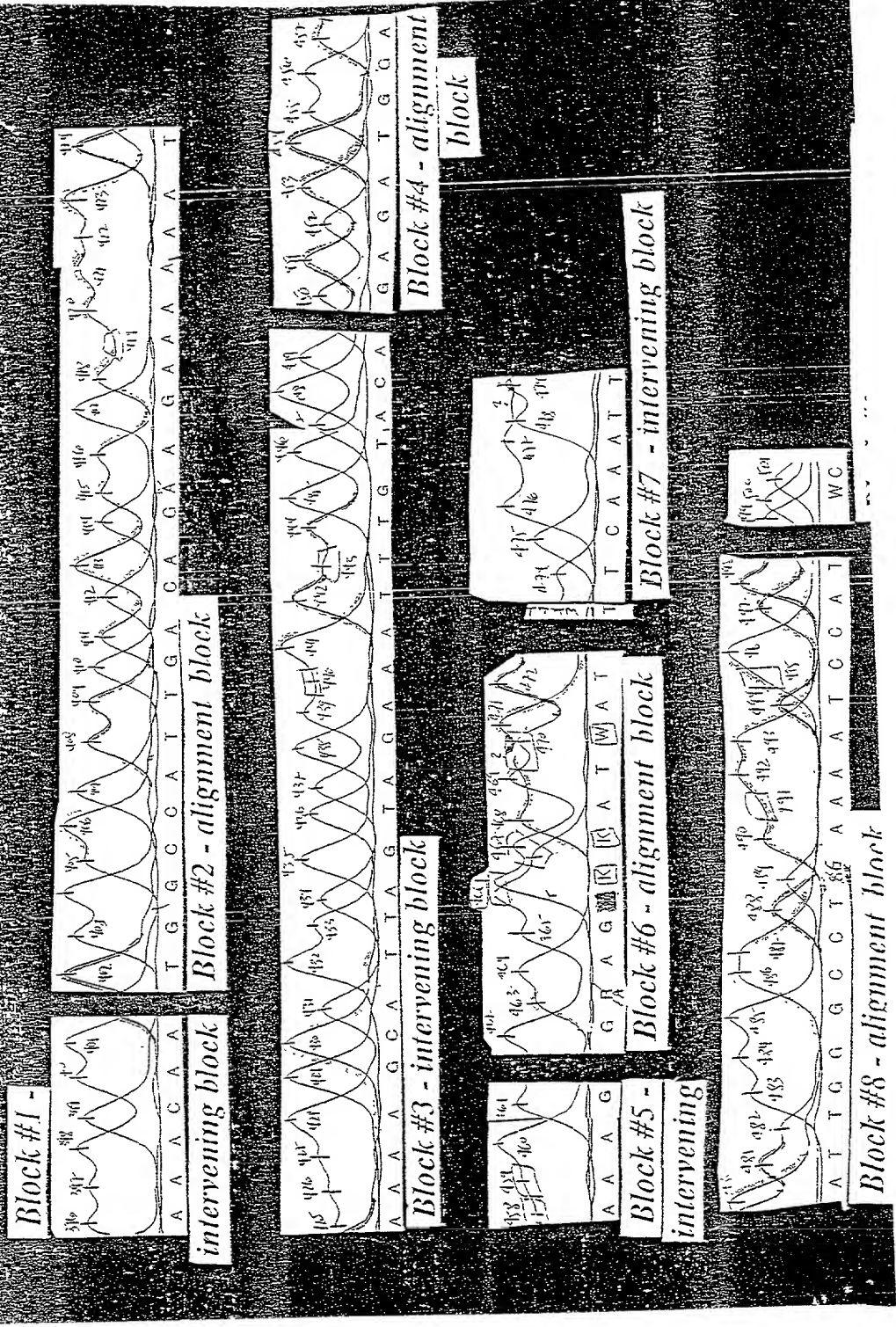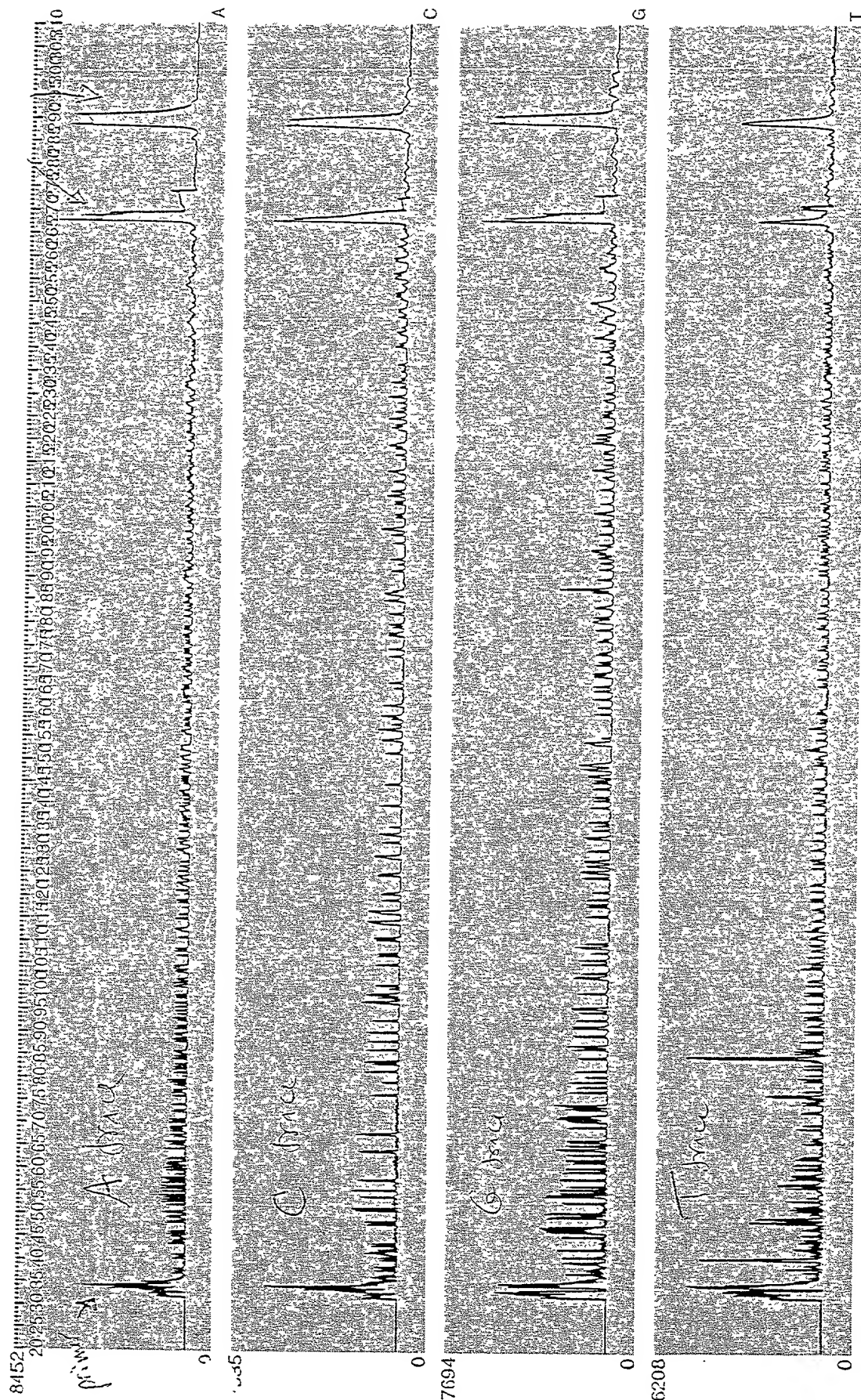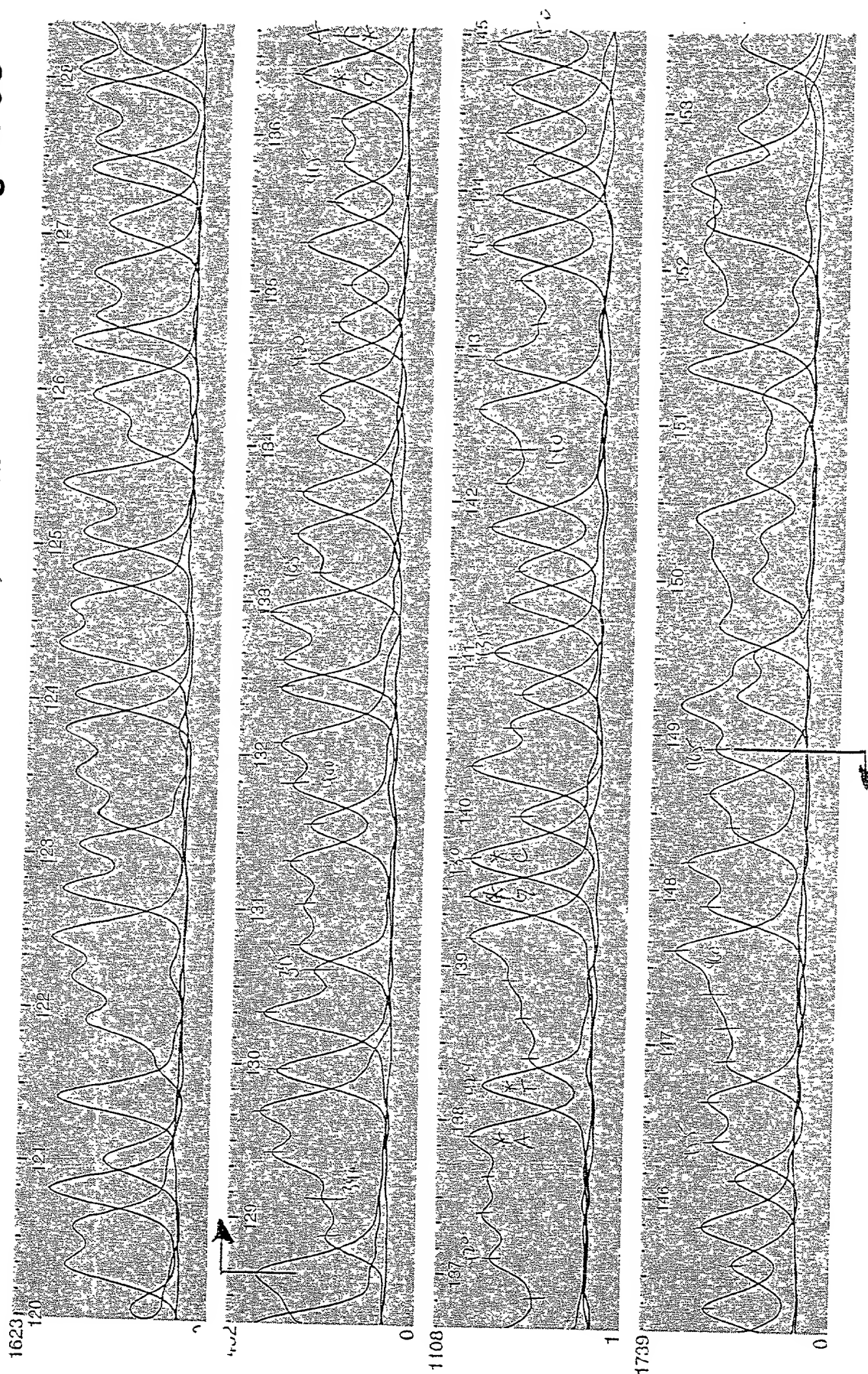
Deviation of the peak position (in number of bases) from the average
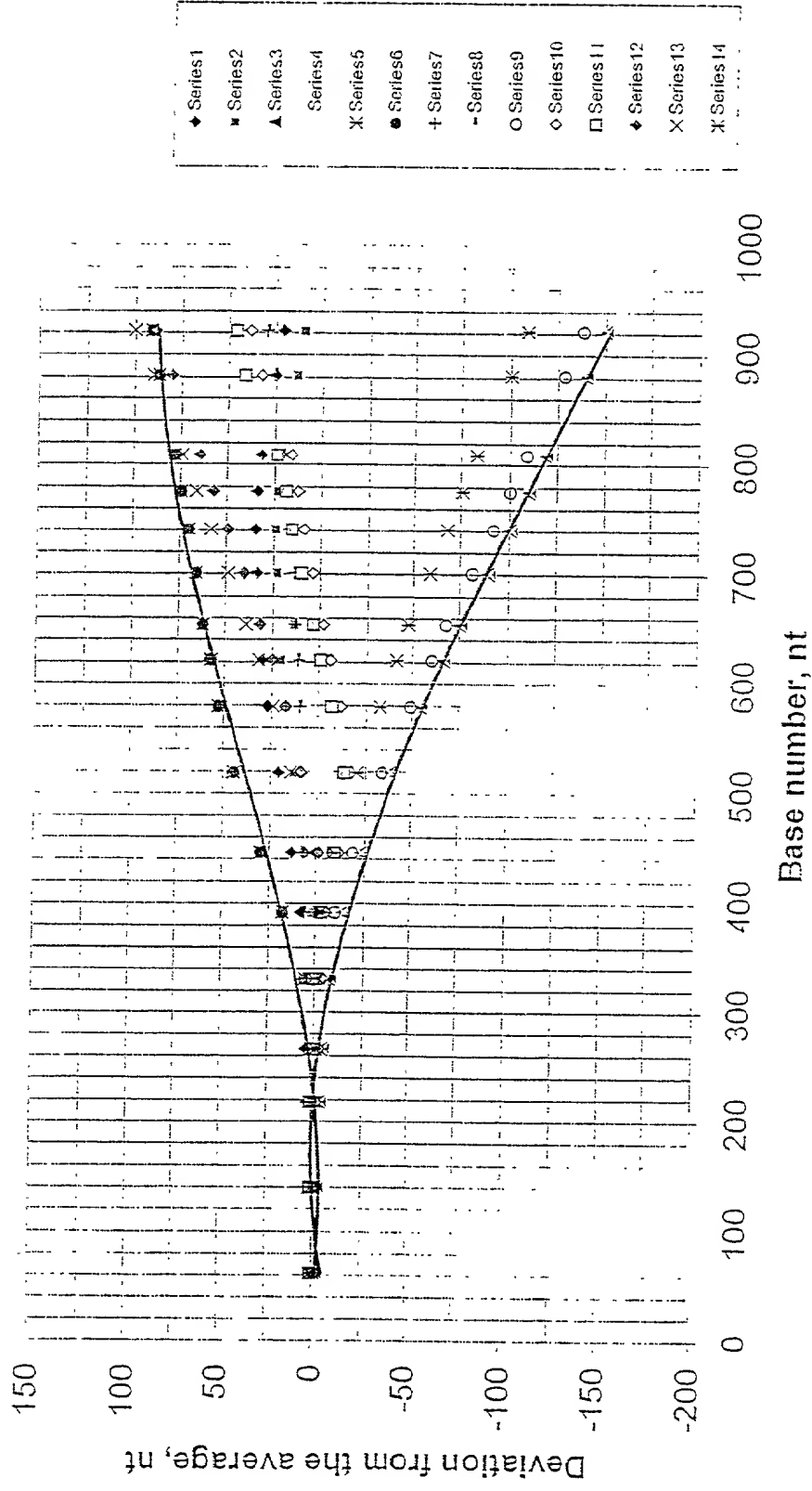as a function of base number in different traces before alignment

Figure 10

Deviation of the peak position (in number of bases) from the average
as a function of base number in the traces aligned with internal
standards
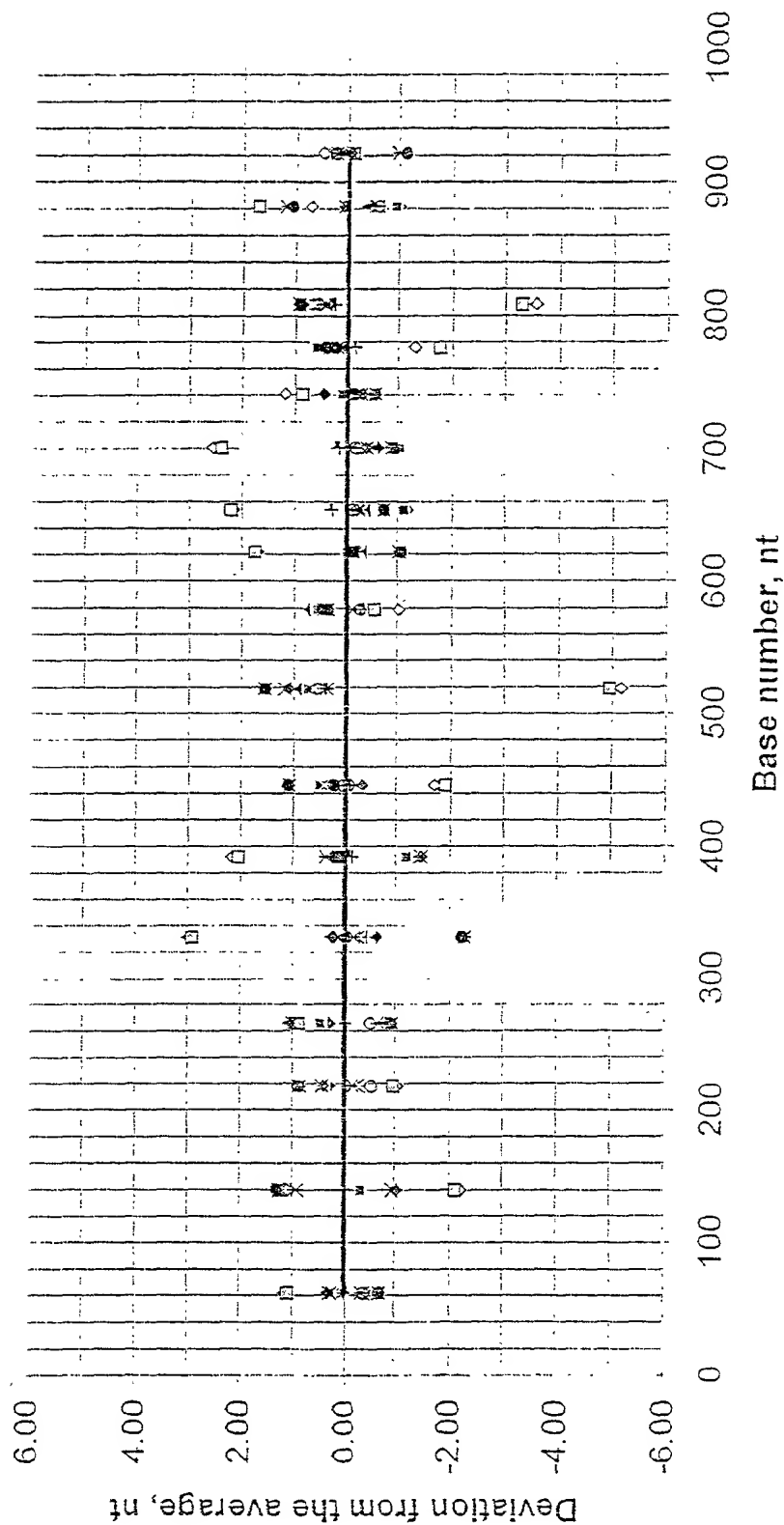
(long gel, M13, 5-th degree polynomial) 17 ref. peaks

Figure 11

Deviation of the peak position from the average as a function of base number in the traces aligned with internal standards (long gel, M13, 6 peaks, 5-th degree polynomial)
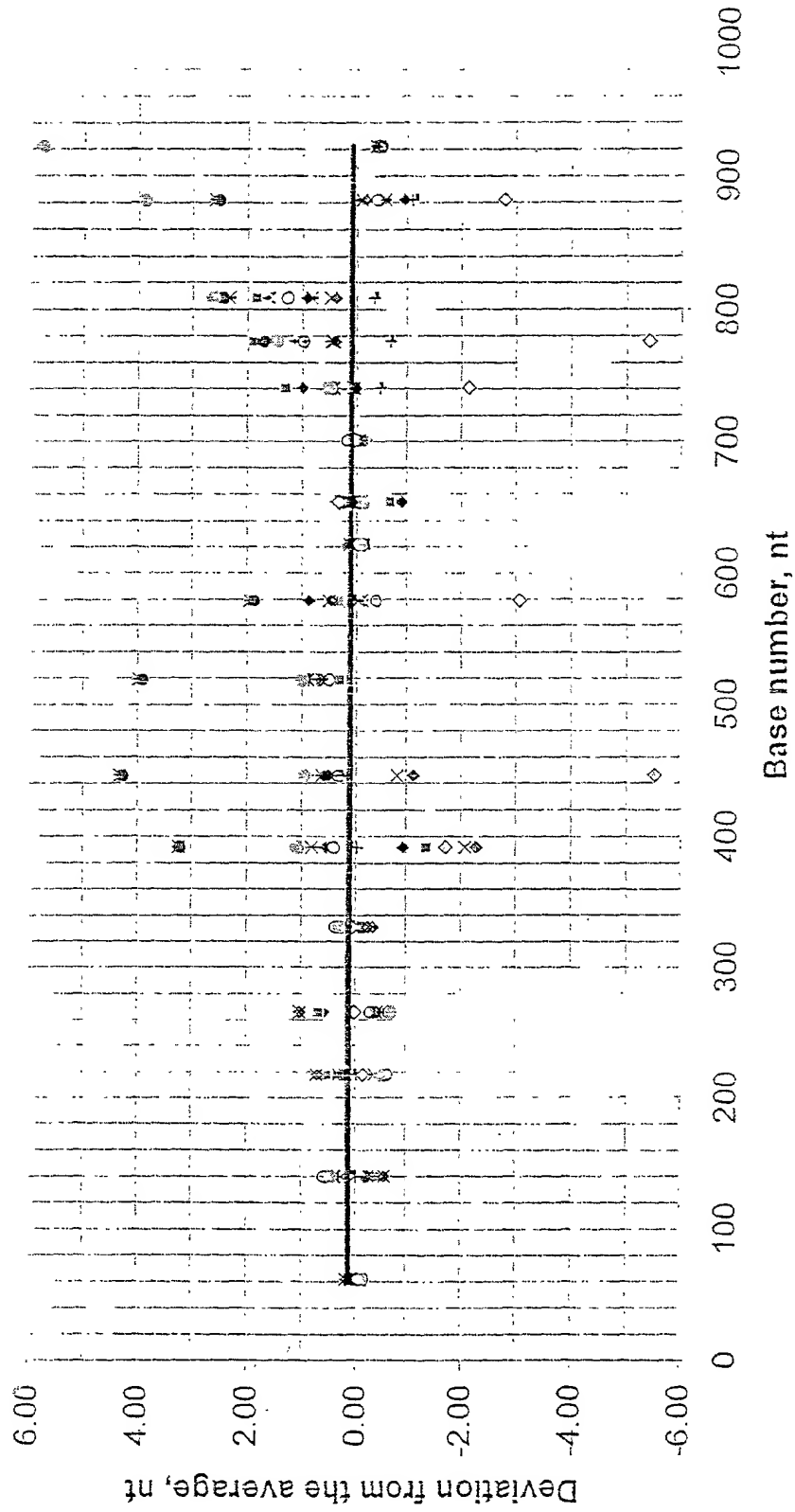

Figure 12